

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lal, Preeti
Corley, Neil C.

(ii) TITLE OF THE INVENTION: HUMAN SHORT CHAIN DEHYDROGENASE

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0475 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSN0T01
(B) CLONE: 356351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Ala Pro Met Asn Gly Gln Val Cys Val Val Thr Gly Ala Ser
 1 5 10 15
 Arg Gly Ile Gly Arg Gly Ile Ala Leu Gln Leu Cys Lys Ala Gly Ala
 20 25 30
 Thr Val Tyr Ile Thr Gly Arg His Leu Asp Thr Leu Arg Val Val Ala
 35 40 45
 Gln Glu Ala Gln Ser Leu Gly Gly Gln Cys Val Pro Val Val Cys Asp
 50 55 60
 Ser Ser Gln Glu Ser Glu Val Arg Thr Leu Phe Glu Gln Val Asp Arg
 65 70 75 80
 Glu Gln Gln Gly Arg Leu Asp Val Leu Val Asn Asn Ala Tyr Ala Gly
 85 90 95
 Val Gln Thr Ile Leu Asn Thr Arg Asn Lys Ala Phe Trp Glu Thr Pro
 100 105 110
 Ala Ser Met Trp Asp Asp Ile Asn Asn Val Gly Leu Arg Gly His Tyr
 115 120 125
 Phe Cys Ser Val Tyr Gly Ala Arg Leu Met Val Pro Ala Gly Gln Gly
 130 135 140
 Leu Ile Val Val Ile Ser Ser Pro Gly Ser Leu Gln Tyr Met Phe Asn
 145 150 155 160
 Val Pro Tyr Gly Val Lys Ala Ala Cys Asp Lys Leu Ala Ala Asp
 165 170 175
 Cys Ala His Glu Leu Arg Arg His Gly Val Ser Cys Val Ser Leu Trp
 180 185 190
 Pro Gly Ile Val Gln Thr Glu Leu Leu Lys Glu His Met Ala Lys Glu
 195 200 205
 Glu Val Leu Gln Asp Pro Val Leu Lys Gln Phe Lys Ser Ala Phe Ser
 210 215 220
 Ser Ala Glu Thr Thr Glu Leu Ser Gly Lys Cys Val Val Ala Leu Ala
 225 230 235 240
 Thr Asp Pro Asn Ile Leu Ser Leu Ser Gly Lys Val Leu Pro Ser Cys
 245 250 255
 Asp Leu Ala Arg Arg Tyr Gly Leu Arg Asp Val Asp Gly Arg Pro Val
 260 265 270
 Gln Asp Tyr Leu Ser Leu Ser Ser Val Leu Ser His Val Ser Gly Leu
 275 280 285
 Gly Trp Leu Ala Ser Tyr Leu Pro Ser Phe Leu Arg Val Pro Lys Trp
 290 295 300
 Ile Ile Ala Leu Tyr Thr Ser Lys Phe
 305 310

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT01
- (B) CLONE: 356351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAACTTTGG	CCTGGGACTC	TGCCCTCTA	CCTCAGCACA	GAATCGCCCC	GGGTCTACT	60
ACAGAATCAA	TCCTTGAACA	CTGCCTCCAC	GTCGCCGGCT	CAATCTGGGC	GAGAACCCAG	120
ACTTCCACCG	CAGCCCCGCA	ATCTGCAGAC	CTCAGCGGCA	GCGCAGGTGG	CAGACCTGCC	180
TCCTTTGCCT	GTGAGTCATG	GCAGCTCCCA	TGAATGGCCA	AGTGTGTGTG	GTGACTGGTG	240

CCTCCAGGGG	TATTGGCCGT	GGCATTGCCT	TGCAGCTCTG	CAAAGCAGGC	GCCACAGTT	300
ACATCACTGG	CCGCCATCTG	GACACCCTTC	GCGTTGTTGC	TCAGGAGGCA	CAATCCCTCG	360
GGGGCAATG	TGTGCCTGTG	GTGTGCGATT	CAAGCCAGGA	GAGTGAAGTG	CGAACGCTGT	420
TTGAGCAAGT	GGATCAGGAA	CAGCAAGGGC	GTCTAGATGT	GCTGGTCAAC	AATGCTTATG	480
CAGGGGTCCA	GACGATCCTG	AAACACCAGGA	ATAAGGCATT	CTGGGAAACC	CCTGCCTCCA	540
TGTGGGATGA	TATCAACAAAC	GTCGGACTCA	GAGGCCACTA	CTTTGCTCA	GTGTATGGGG	600
CACGGCTGAT	GGTACCAAGCT	GGCCAGGGC	TCATCGTGGT	CATCTCCTCC	CCAGGAAGCC	660
TGCAGTATAT	GTTCAATGTC	CCCTATGGTG	TGGGAAAGC	TGCGTGTGAC	AAGCTGGCTG	720
CTGACTGTGC	CCACGAGCTG	CGGCGCCATG	GGGTCAGCTG	TGTGTCTCTG	TGGCCGGGGA	780
TTGTGCAGAC	AGAACTGCTG	AAGGAGCATA	TGGCAAAGGA	GGAGGTCCTG	CAGGATCCTG	840
TGTTGAAGCA	GTTCAAATCA	GCCTTCTCAT	CTGCAGAAAC	CACAGAATTG	AGTGGCAAAT	900
GTGTGGTGGC	TTTGGCAACA	GATCCAATA	TCCTGAGCCT	GAGTGGTAAG	GTGCTGCCAT	960
CCTGTGACCT	TGCTCGACGC	TATGGCCTTC	GGGATGTGGA	CGGCCGCCCC	GTCCAAGACT	1020
ATTGTCTTT	GAGCTCTGTT	CTCTCACACG	TGTCCGGCCT	GGCCTGGCTG	GCCTCCTTAC	1080
TGCCCTCCTT	CCTCCGTGTG	CCCAAGTGGA	TTATTGCCCT	CTACACTAGC	AAGTTCTAAC	1140
CCTCCTGGTC	TGACACTACG	TCTCTGCTTG	TCTTCTCATT	TGGACTTGTT	GGTCGTCCT	1200
GTCTCAGTGA	AACAGCAGCC	TTTCTGTGTT	ACCCATACCC	TTGATATGAA	GAGAAGCCCT	1260
CTGCTGTGTG	TCCGTGGTGA	GTTCCTGGGT	GGCCCTAGGT	CCCTTCCTTTC	TGCCTTGGTT	1320
TCCCTTGTCC	TTCTTTTAC	TTTTTGCCTT	AGTATTGAAA	AATGCTCTTG	GAGCTAATAA	1380
					AAGTCTA	1387

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2315796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Val	Ile	Leu	Gln	Asp	Gln	Val	Ala	Leu	Val	Thr	Gly	Ala	Ser
1				5				10					15		
Arg	Gly	Ile	Gly	Arg	Gly	Ile	Ala	Leu	Gln	Leu	Gly	Glu	Ala	Gly	Ala
							20			25			30		
Thr	Val	Tyr	Ile	Thr	Gly	Arg	Arg	Pro	Glu	Leu	Ser	Asp	Asn	Phe	Arg
							35			40			45		
Leu	Gly	Leu	Pro	Ser	Leu	Asp	Tyr	Val	Ala	Lys	Glu	Ile	Thr	Ser	Arg
							50			55			60		
Gly	Gly	Lys	Gly	Ile	Ala	Leu	Tyr	Val	Asp	His	Ser	Asn	Met	Thr	Glu
							65			70			75		80
Val	Lys	Phe	Leu	Phe	Glu	Lys	Ile	Lys	Glu	Asp	Glu	Glu	Gly	Lys	Leu
							85			90			95		
Asp	Ile	Leu	Val	Asn	Asn	Val	Tyr	Asn	Ser	Leu	Gly	Lys	Ala	Thr	Glu
							100			105			110		
Met	Ile	Gly	Lys	Thr	Phe	Phe	Asp	Gln	Asp	Pro	Ser	Phe	Trp	Asp	Asp
							115			120			125		
Ile	Asn	Gly	Val	Gly	Leu	Arg	Asn	His	Tyr	Tyr	Cys	Ser	Val	Tyr	Ala
							130			135			140		
Ala	Arg	Met	Met	Val	Glu	Arg	Arg	Lys	Gly	Leu	Ile	Val	Asn	Val	Gly
							145			150			155		160
Ser	Leu	Gly	Gly	Leu	Lys	Tyr	Val	Phe	Asn	Val	Ala	Tyr	Gly	Ala	Gly
							165			170			175		
Lys	Glu	Ala	Leu	Ala	Arg	Met	Ser	Thr	Asp	Met	Ala	Val	Glu	Leu	Asn
							180			185			190		

Pro Tyr Asn Val Cys Val Val Thr Leu Ile Pro Gly Pro Val Lys Thr
195 200 205
Glu Thr Ala Asn Arg Thr Ile Ile Asp Asp Ala Tyr Lys Met Ile Lys
210 215 220
Glu Asn Pro Glu Leu Glu Glu Phe Ile Lys Gly Glu Ser Thr Glu Tyr
225 230 235 240
Thr Gly Lys Ala Leu Ala Arg Leu Ala Met Asp Pro Gly Lys Leu Lys
245 250 255
Lys Ser Gly Lys Thr Leu Phe Thr Glu Asp Leu Ala Gln Lys Tyr Asp
260 265 270
Phe Ser Asp Lys His Gly Ala Gly Met Glu Pro Gln Asn Ile Arg Ser
275 280 285
Ile Arg Thr Ile Leu Gly Thr Met Gly Lys Glu Glu Val Ala Lys Tyr
290 295 300
Ile Pro Pro Gln Ile Lys Leu Pro Lys Trp Val Ile Trp Gln Ser Val
305 310 315 320
Asn Arg Phe